

## SEQUENCE LISTINGS

## (1) GENERAL INFORMATION

## (i) APPLICANT:

SHAUGNESSEY, Stephen  
72 Leaside Drive  
St. Catharines, Ontario  
CANADA

AUSTIN, Richard Carl  
68 Rosemary Lane  
Ancaster, Ontario  
CANADA

## (ii) TITLE OF INVENTION: OSTEOPOROSIS TREATMENT

## (iii) NUMBER OF SEQUENCES: 10

## (iv) CORRESPONDENCE ADDRESS:

RIDOUT & MAYBEE  
150 Metcalfe St.  
Ottawa, Ontario K2P 0J7  
CANADA

## (v) COMPUTER READABLE FORM

- (a) COMPUTER: IBM Compatible  
(b) OPERATING SYSTEM: WINDOWS 95  
(c) SOFTWARE: WORDPERFECT 8

## (vi) CURRENT APPLICATION DATA

- (a) APPLICATION NUMBER: 2,237,915  
(b) FILING DATE: 1998/05/19

(c) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(a) APPLICATION NUMBER: NONE

(b) FILING DATE:

(c) CLASSIFICATION:

(viii) PATENT AGENT INFORMATION

(a) NAME: Robert G. Hirons, RIDOUT & MAYBEE

(b) REFERENCE NUMBER: 29210-0011

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 20

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: human interleukin-11 receptor protein sequence

(vii) IMMEDIATE SOURCE: synthetic

(viii) POSITION IN GENOME:

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(a) CHROMOSOME/SEGMENT: 9p13

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY: IL-11 binding region

(b) LOCATION: amino acids 1-8

(c) IDENTIFICATION METHOD: experiment

(d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

(c) JOURNAL:

(d) VOLUME:

(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO:

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO:1

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Arg Arg Leu Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu

(3) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 20

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: human interleukin-11 receptor protein sequence

(vii) IMMEDIATE SOURCE: synthetic

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT: 9p13

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY:

(b) LOCATION:

(c) IDENTIFICATION METHOD:

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(d) OTHER INFORMATION:

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

(c) JOURNAL:

(d) VOLUME:

(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO:

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO:2

Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr

(4) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 1140 bases

(b) TYPE: nucleotide and amino acid

(c) STRANDEDNESS: double stranded

(d) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA, protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE: murine interleukin-11 receptor sequence

(vii) IMMEDIATE SOURCE: mouse bone marrow stromal cells

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT:

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY:

(b) LOCATION:

(c) IDENTIFICATION METHOD: experiment

(d) OTHER INFORMATION: soluble form of IL-11 receptor, sequence additionally modified from wild type for cloning and histidine purification purposes

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

(c) JOURNAL:

(d) VOLUME:

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(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO: 3

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO:3

54                    9                    18                    27                    36                    45

5' ATG AGC AGC AGC TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT  
ACG GCC

Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala  
Thr Ala

63                    72                    81                    90                    99

108

CTG GTG TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG  
GTC CAG

Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val  
Gln

117                    126                    135                    144                    153

162

TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT  
GCT GGG

Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser  
Ala Gly

171                    180                    189                    198                    207

216

ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC CAG GGA

CCT GAC

Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu Gln Gly Pro  
Asp

225 234 243 252 261  
270

TCT GGG TTA GGA CAC AAA CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT  
GAA GGC

Ser Gly Leu Gly His Lys Leu Val Leu Ala Gln Val Asp Ser Pro Asp  
Glu Gly

279 288 297 306 315  
324

ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC  
CTG AAG

Thr Tyr Val Cys Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys  
333 342 351 360 369

378  
CTG GGC TTT CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC  
TAT GAA

Leu Gly Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp  
Tyr Glu

387 396 405 414 423  
432

AAC TTC TCC TGT ACT TGG AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC  
CGC TAC

Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg  
Tyr

441 450 459 468 477  
486

CTT ACT TCC TAC AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG  
GAA AGT

Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser

495 504 513 522 531



540

CCA TCC ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC  
CGA TGT

Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys

549

558

567

576

585

594

GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC  
GAG GTG

Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr  
Glu Val

603

612

621

630

639

648

AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA CAG AGC  
ATC TTG

Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu Gln Ser  
Ile Leu

657

666

675

684

693

702

CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC GTA CCT AGT TAC  
CCG AGA

Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Ser Tyr  
Pro Arg

711

720

729

738

747

756

CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC TCC TGG CGT CGC CAA CCC  
CAC TTT

Arg Leu His Ala Ser Trp Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro  
His Phe

765

774

783

792

801

810

CTG CTC AAG TTC CGG TTG CAA TAC CGA CCA GCA CAG CAT CCA GCG TGG  
TCC ACG

Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr

819

828

837

846

855

864

GTG GAG CCC ATT GGC TTG GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG  
CTG CCA

Val Glu Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro

873

882

891

900

909

918

CAC GCG GTA CGA GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG  
AGC GCC

His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp  
Ser Ala

927

936

945

954

963

972

TGG AGC CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT  
GAG ATA

Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp  
Glu Ile

981

990

999

1008

1017

1026

CCT GAT TGG AGC CAG GGA CAC GGA CAG CAG CTA GAG GCA GTA GTA GCT  
CAG GAG

Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala  
Gln Glu

1035

1044

1053

1062

1071

1080

GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA AGG CCA  
CTT GAT

Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro Arg Pro Leu  
Asp

1089

1098

1107

1116

1125

1134

CAC AGG GAT CCC TTG GAG CAA CTG GTG CCA CGC GGT TCT CAC CAC CAC  
CAC CAC

His Arg Asp Pro Leu Glu Gln Leu Val Pro Arg Gly Ser His His His His  
His

1140  
CAC TGA 3'

His \*\*\*

(5) INFORMATION FOR SEQ ID NO:4

(1) SEQUENCE CHARACTERISTICS

(1) LENGTH: 10

(2) TYPE: amino acid

(3) STRANDEDNESS:

(4) TOPOLOGY: linear

(2) MOLECULE TYPE: peptide

(3) HYPOTHETICAL: yes

(4) ANTISENSE: no

(5) FRAGMENT TYPE: internal

(6) ORIGINAL SOURCE: human interleukin-11 receptor protein sequence

(7) IMMEDIATE SOURCE: synthetic

(8) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT: 9p13

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

- (a) NAME/KEY: ineffectual gp130 binding region
- (b) LOCATION: entire sequence
- (c) IDENTIFICATION METHOD: experiment
- (d) OTHER INFORMATION:

(x) PUBLICATION INFORMATION

- (a) AUTHOR(S):
- (b) TITLE:
- (c) JOURNAL:
- (d) VOLUME:
- (e) ISSUE:
- (f) PAGES:
- (g) DATE:
- (h) DOCUMENT NUMBER:
- (i) FILING DATE:
- (j) PUBLICATION DATE:
- (k) RELEVANT RESIDUES IN SEQUENCE ID NO:

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 4

Gly Asp Val Ala Asp Leu Pro Tyr Ala Leu

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS

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- (a) LENGTH: 7
- (b) TYPE: amino acid
- (c) STRANDEDNESS:
- (d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: human interleukin-11 receptor protein sequence

(vii) IMMEDIATE SOURCE: synthetic

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT: 9p13

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

- (a) NAME/KEY: IL-11 binding region
- (b) LOCATION: entire sequence
- (c) IDENTIFICATION METHOD: experiment
- (d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

- (b) TITLE:
- (c) JOURNAL:
- (d) VOLUME:
- (e) ISSUE:
- (f) PAGES:
- (g) DATE:
- (h) DOCUMENT NUMBER:
- (i) FILING DATE:
- (j) PUBLICATION DATE:
- (k) RELEVANT RESIDUES IN SEQUENCE ID NO:

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO:5

Arg Arg Leu Arg Ala Ser Trp

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS

- (a) LENGTH: 20
  - (b) TYPE: amino acid
  - (c) STRANDEDNESS:
  - (d) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: no
  - (iv) ANTISENSE: no
  - (v) FRAGMENT TYPE: internal
-

(vi) ORIGINAL SOURCE: human interleukin-11 receptor protein sequence

(vii) IMMEDIATE SOURCE: synthetic

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT: 9p13

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY: IL-11 binding region

(b) LOCATION:

(c) IDENTIFICATION METHOD: experiment

(d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

(c) JOURNAL:

(d) VOLUME:

(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

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(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO:

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 6

Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 7

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: yes

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT:

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

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- (a) NAME/KEY: IL-11 binding region
- (b) LOCATION:
- (c) IDENTIFICATION METHOD: experiment, homology
- (d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

- (a) AUTHOR(S):
- (b) TITLE:
- (c) JOURNAL:
- (d) VOLUME:
- (e) ISSUE:
- (f) PAGES:
- (g) DATE:
- (h) DOCUMENT NUMBER:
- (i) FILING DATE:
- (j) PUBLICATION DATE:
- (k) RELEVANT RESIDUES IN SEQUENCE ID NO: 7

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 7

Arg Arg Leu X Ala Ser Trp where X is a basic amino acid

(9) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS

- (a) LENGTH: 20
-

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: murine interleukin-11 receptor

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT:

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY: IL-11 binding region

(b) LOCATION:

(c) IDENTIFICATION METHOD: experiment, homology

(d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

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(c) JOURNAL:

(d) VOLUME:

(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO: 8

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 8

Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Ser Tyr Pro

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 20

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: yes

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

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(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT:

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

(a) NAME/KEY:

(b) LOCATION:

(c) IDENTIFICATION METHOD:

(d) OTHER INFORMATION:

(x) PUBLICATION INFORMATION

(a) AUTHOR(S):

(b) TITLE:

(c) JOURNAL:

(d) VOLUME:

(e) ISSUE:

(f) PAGES:

(g) DATE:

(h) DOCUMENT NUMBER:

(i) FILING DATE:

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(j) PUBLICATION DATE:

(k) RELEVANT RESIDUES IN SEQUENCE ID NO: 9

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 9

Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro xxx Tyr Pro  
where xxx is a suitable amino acid

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS

(a) LENGTH: 7

(b) TYPE: amino acid

(c) STRANDEDNESS:

(d) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: murine IL-11 receptor

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(a) CHROMOSOME/SEGMENT:

(b) MAP POSITION:

(c) UNITS:

(ix) FEATURE

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- (a) NAME/KEY: IL-11 binding region
- (b) LOCATION: entire sequence
- (c) IDENTIFICATION METHOD: experiment and homology
- (d) OTHER INFORMATION: IL-11 receptor antagonist

(x) PUBLICATION INFORMATION

- (a) AUTHOR(S):
- (b) TITLE:
- (c) JOURNAL:
- (d) VOLUME:
- (e) ISSUE:
- (f) PAGES:
- (g) DATE:
- (h) DOCUMENT NUMBER:
- (i) FILING DATE:
- (j) PUBLICATION DATE:
- (k) RELEVANT RESIDUES IN SEQUENCE ID NO: 10

(xi) SEQUENCE DESCRIPTION: SEQUENCE ID NO: 10

Arg Arg Leu His Ala Ser Trp

Sub  
A1  
Cont